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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/581,528D

DATE: 05/21/2002

TIME: 10:34:10

Input Set : A:\P19743.ST25.txt

Output Set: N:\CRF3\05212002\I581528D.raw

ENTERED

3 <110> APPLICANT: TAKEDA, Masatoshi  
4 TAKEDA, Junji  
6 <120> TITLE OF INVENTION: Gene Mutant Animals  
8 <130> FILE REFERENCE: P19743  
10 <140> CURRENT APPLICATION NUMBER: 09/581,528D  
11 <141> CURRENT FILING DATE: 1999-01-07  
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00015  
14 <151> PRIOR FILING DATE: 1999-01-07  
16 <160> NUMBER OF SEQ ID NOS: 17  
18 <170> SOFTWARE: PatentIn version 3.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 467  
22 <212> TYPE: PRT  
23 <213> ORGANISM: Human  
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30 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn  
31 20 25 30  
33 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu  
34 35 40 45  
36 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu  
37 50 55 60  
39 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys  
40 65 70 75 80  
42 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val  
43 85 90 95  
45 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln  
46 100 105 110  
48 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg  
49 115 120 125  
51 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val  
52 130 135 140  
54 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys  
55 145 150 155 160  
57 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe  
58 165 170 175  
60 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala  
61 180 185 190  
63 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val  
64 195 200 205  
66 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala  
67 210 215 220

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69 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
70 225                230                235                240
72 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
73                245                250                255
75 Asp Leu Asp Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
76                260                265                270
78 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
79                275                280                285
81 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
82                290                295                300
84 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
85 305                310                315                320
87 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
88                325                330                335
90 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
91                340                345                350
93 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
94                355                360                365
96 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
97                370                375                380
99 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
100 385                390                395                400
102 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
103                405                410                415
105 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
106                420                425                430
108 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
109                435                440                445
111 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
112                450                455                460
114 Phe Tyr Ile
115 465

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117 &lt;210&gt; SEQ ID NO: 2

118 &lt;211&gt; LENGTH: 1404

119 &lt;212&gt; TYPE: DNA

120 &lt;213&gt; ORGANISM: Human

122 &lt;400&gt; SEQUENCE: 2

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123 atgacagagt tacctgcacc gttgtcctac ttccagaatg cacagatgtc tgaggacaac      60
125 cacctgagca atactgtacg tagccagaat gacaatagag aacggcagga gcacaacgac      120
127 agacggagcc ttggccaccc tgagccatta tctaattggac gaccccaggg taactcccgg      180
129 caggtggttg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag      240
131 catgtgatca tgcctctttgt cctgtgtact ctctgcatgg tgggtggtcgt ggctactatt      300
133 aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa      360
135 gataccgaga ctgtggggcca gagagccctg cactcaattc tgaatgctgc catcatgac      420
137 agtgtcattg ttgtcatgac tatcctcctg gtggttctgt ataaatacag gtgctataag      480
139 gtcattccatg cctggccttat tatatcatct ctattgttgc tgttcttttt ttcattcatt      540
141 tacttggggg aagtgtttta aacctataac gttgctgtgg actacattac tgttgcactc      600
143 ctgatctgga attttgggtg ggtgggaatg atttccattc actggaaagg tccacttcga      660
145 ctccagcagg catatctcat tatgattagt gccctcatgg ccttgggtgt tatcaagtac      720

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147 ctccctgaat ggactgcgtg gctcatcttg gctgtgattt cagtatatga tttagtggct 780
149 gttttgtgtc cgaaaggtec acttcgtatg ctggttgaaa cagctcagga gagaaatgaa 840
151 acgctttttc cagctctcat ttactcctca acaatggtgt ggttggtgaa tatggcagaa 900
153 ggagacccgg aagetcaaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca 960
155 gaaagggagt cacaagacac tctagggcct cctcgtctta cactgagtc acgagctgct 1020
157 gaagcccaga gggacagtea tctagggcct cctcgtctta cactgagtc acgagctgct 1080
159 qtccaggaac ttccagcag tatcctcgtt ggtgaagacc cagaggaag gggagtaaaa 1140
161 cttggattgg gagatttcat ttctacagt gttctggttg gtaaaacctc agcaacagcc 1200
163 agtggagact ggaacacaa ctagacctgt ttctagcca tattaattgg tttgtgctt 1260
165 acattattac tcttgccat ttccaagaaa gcattgccag ctcttccaat ctccatcacc 1320
167 tttgggcttg tttctactt tgccacagat tatctgtac agccttttat ggaccaatta 1380
169 gcattccatc aattttatat ctac 1404
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 467
174 <212> TYPE: PRT
175 <213> ORGANISM: Mouse
177 <400> SEQUENCE: 3
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180 1 5 10 15
182 Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
183 20 25 30
185 Glu Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
186 35 40 45
188 Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
189 50 55 60
191 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
192 65 70 75 80
194 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
195 85 90 95
197 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
198 100 105 110
200 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
201 115 120 125
203 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
204 130 135 140
206 Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
207 145 150 155 160
209 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
210 165 170 175
212 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
213 180 185 190
215 Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
216 195 200 205
218 Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
219 210 215 220
221 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
222 225 230 235 240
224 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
225 245 250 255

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227 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
228           260           265           270
230 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
231           275           280           285
233 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
234           290           295           300
236 Ala Glu Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
237 305           310           315           320
239 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
240           325           330           335
242 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
243           340           345           350
245 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
246           355           360           365
248 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
249           370           375           380
251 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
252 385           390           395           400
254 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
255           405           410           415
257 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
258           420           425           430
260 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
261           435           440           445
263 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
264           450           455           460
266 Phe Tyr Ile
267 465

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269 &lt;210&gt; SEQ ID NO: 4

270 &lt;211&gt; LENGTH: 1404

271 &lt;212&gt; TYPE: DNA

272 &lt;213&gt; ORGANISM: Mouse

274 &lt;400&gt; SEQUENCE: 4

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277 cactccagca gggccatccg gagccagaat gacagccaag aacggcagca gcagcatgac      120
279 aggcagagac ttgacaaccc tgagccaata tctaattggc gggcccagag taactcaaga      180
281 caggtggtgg aacaagatga ggaggaagac gaagagctga cattgaaata tggagccaag      240
283 catgtcatca tgccttttgt ccccgtagcc ctctgcatgg tctctgtctg ggcaccatc      300
285 aaatcagtea gcttctatac ccggaaggac ggtcagctaa tctacacccc attcacagaa      360
287 gacactgaga ctgtaggcca aagagccctg cactcgatcc tgaatgcggc catcatgac      420
289 agtgtcattg tcattatgac cactctcctg gtggtcctgt ataaatacag gtgtacaag      480
291 gtcatecaac cctggtttat tatttcatct ctgttggttg tgttcttttt ttctttcatt      540
293 tacttagggg aagtatttaa gacctacaat gtgcgcgtgg actacgttac agtagcactc      600
295 ctaatctgga attttggtgt ggtcgggatg attgccatcc actggaaagg ccccttcga      660
297 ctgcagcagg cgtatctcat tatgatcagt gccctcatgg ccttggtatt tatcaagtac      720
299 ctcccgaat ggaccgcatg gctcatcttg ctgtgattt cagtatatga tttggtgget      780
301 gttttatgtc ccaaaggccc acttcgtatg ctggttgaaa cagctcagga aagaaatgag      840
303 actctctttc cagctcttat ctattcttca acaatggtgt ggttggtgaa tatggtgaa      900
305 ggagacccag aagcccaaag gagggtagcc aagaacccca agtataacac acaaagagcg      960

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307 gagagaaqaga cacaggacag tggttctggg aacgatgatg gtggcttcag tgaggagtgg 1020
309 gaggeccaaa gagacagtea cctggggcct categetcca ctcccagtc aagagctgct 1080
311 gtccaggaac tttctgggag cattctaacg agtgaagacc cggaggaaaag aggagtaaaa 1140
313 cttggactgg gagatttcat tttctacagt gttctgggtg gtaaggcctc agcaaccgcc 1200
315 agtggagact ggaacacaac catagcctgc tttgtagcca tactgatcg cctgtgcctt 1260
317 acattaactcc tgcctgccat tttcaagaaa gcgttgccag cctcccccat ctccatcacc 1320
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321 gcattccatc agttttatat ctac 1404
324 <210> SEQ ID NO: 5
325 <211> LENGTH: 25
326 <212> TYPE: DNA
C--> 327 <213> ORGANISM: Artificial
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Primer
332 <400> SEQUENCE: 5
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336 <210> SEQ ID NO: 6
337 <211> LENGTH: 23
338 <212> TYPE: DNA
C--> 339 <213> ORGANISM: Artificial
341 <220> FEATURE:
342 <223> OTHER INFORMATION: Primer
344 <400> SEQUENCE: 6
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349 <211> LENGTH: 36
350 <212> TYPE: DNA
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353 <220> FEATURE:
354 <223> OTHER INFORMATION: Primer
356 <400> SEQUENCE: 7
357 tgtggtcggg atgategcca cccactggaa aggcc 36
360 <210> SEQ ID NO: 8
361 <211> LENGTH: 36
362 <212> TYPE: DNA
C--> 363 <213> ORGANISM: Artificial
365 <220> FEATURE:
366 <223> OTHER INFORMATION: Primer
368 <400> SEQUENCE: 8
369 gggcctttcc agtgggtggc gatcatcccg accaca 36
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373 <211> LENGTH: 18
374 <212> TYPE: DNA
C--> 375 <213> ORGANISM: Artificial
377 <220> FEATURE:
378 <223> OTHER INFORMATION: Primer
380 <400> SEQUENCE: 9
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384 <210> SEQ ID NO: 10

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